Sub H2

69. The method of claim 68, further comprising isolating said vector from those host cells which have undergone a lytic event.

70. The method of claim 68, further comprising:

(a) isolating said vector from those host cells which have undergone a lytic event;

Sub E2

(b) transferring said vector to a population of host cells, wherein said vector is capable of facilitating expression of said target epitope in said host cells, and wherein said host cells express a defined MHC molecule;

(c) contacting said host cells with cytotoxic T-lymphocytes specific for said target epitope and restricted for said MHC molecule, under conditions wherein a host cell expressing said target epitope will undergo a lytic event upon contact with said T-lymphocytes; and

(d) recovering those host cells which have undergone a lytic event.

71. The method of claim 68, wherein said vector is a virus.

72. The method of claim 71, wherein said vector is a virus capable of producing infectious viral particles in eukaryotic cells.

73. The method of claim 72, wherein the naturally-occurring genome of said virus is linear, double stranded DNA.

74. The method of claim 72, wherein said vector is a virus capable of producing infectious viral particles in mammalian cells.

75. The method of claim 74, wherein the naturally-occurring genome of said virus is linear, double-stranded DNA.

76. The method of claim 72, wherein said vector is a poxvirus vector.

77. The method of claim 76, wherein said vector is a vaccinia virus vector.

78. The method of claim 71, wherein said host cells are permissive for the production of infectious viral particles of said virus.

79. The method of claim 76, wherein said vector further comprises a transcriptional control region in operable association with said heterologous nucleic acid molecules, and wherein said transcriptional control region functions in a poxvirus.

80. The method of claim 79, wherein said transcriptional control region comprises a promoter.

81. The method of claim 80, wherein said promoter is constitutive.

82. The method of claim 80, wherein said promoter is a vaccinia virus p7.5 promoter.

83. The method of claim 82, wherein said vector comprises the sequence shown in SEQ ID NO:1.

84. The method of claim 80, wherein said promoter is a synthetic early/late promoter.

85. The method of claim 84, wherein said vector comprises the sequence shown in SEQ ID NO:3.

D1

Sub E47

86. The method of claim 79, wherein said transcriptional control region comprises a transcriptional termination region.

87. The method of claim 79, wherein said vector further comprises a translational control region associated with said transcriptional control region.

88. The method of claim 87, wherein said vector comprises the sequence shown in SEQ ID NO:6.

Sub E57

89. The method of claim 87, wherein said translational control region comprises a translation initiation codon operably linked to said heterologous nucleic acid molecules.

90. The method of claim 89, wherein said translation initiation codon occurs in one of three reading frames.

91. The method of claim 90, wherein said vector comprises a sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:8 and SEQ ID NO:9.

92. The method of claim 68, wherein said library of heterologous nucleic acid molecules is isolated from a tumor cell, and wherein said target epitope is differentially expressed in said tumor cell relative to a non-tumorigenic counterpart cell.

93. The method of claim 92, wherein said heterologous nucleic acid molecules are cDNA molecules synthesized from said tumor cell.

~~94. The method of claim 73, wherein said library is constructed by a method comprising:~~

~~(a) cleaving an isolated linear DNA virus genome to produce a first viral fragment and a second viral fragment, wherein said first fragment is nonhomologous with said second fragment;~~

~~(b) providing a population of transfer plasmids comprising said heterologous nucleic acid molecules flanked by a 5' flanking region and a 3' flanking region, wherein said 5' flanking region is homologous to said first viral fragment and said 3' flanking region is homologous to said second viral fragment; and wherein said transfer plasmids are~~

capable of homologous recombination with said first and second viral fragments such that a viable virus genome is formed;

(c) introducing said transfer plasmids and said first and second viral fragments into a host cell under conditions wherein a transfer plasmid and said viral fragments undergo *in vivo* homologous recombination, thereby producing a viable modified virus genome comprising a heterologous nucleic acid molecule; and

(d) recovering said modified virus genome.

D1

95. The method of claim 94, wherein said virus genome comprises a first recognition site for a first restriction endonuclease and a second recognition site for a second restriction endonuclease; and ~~wherein~~ said first and second viral fragments are produced by digesting said viral genome with said first restriction endonuclease and said second restriction endonuclease, and isolating said first and second viral fragments.

96. The method of claim 95, wherein said first and second recognition sites are physically arranged in said genome such that the region extending between said first and second viral fragments is not essential for virus infectivity.

97. The method of claim 94, wherein said modified virus genome is packaged in an infectious viral particle.

Sub H5

98. The method of claim 75, wherein said library is constructed by a method comprising:

(a) cleaving an isolated linear DNA virus genome to produce a first viral fragment and a second viral fragment, wherein said first fragment is nonhomologous with said second fragment;

(b) providing a population of transfer plasmids comprising said heterologous nucleic acid molecules flanked by a 5' flanking region and a 3' flanking region, wherein said 5' flanking region is homologous to said first viral fragment and said 3' flanking region is homologous to said second viral fragment; and wherein said transfer plasmids are capable of homologous recombination with said first and second viral fragments such that a viable virus genome is formed;

Sub B6

(c) introducing said transfer plasmids and said first and second viral fragments into a host cell under conditions wherein a transfer plasmid and said viral fragments undergo *in vivo* homologous recombination, thereby producing a viable modified virus genome comprising a heterologous nucleic acid molecule; and

(d) recovering said modified virus genome.

99. The method of claim 98, wherein said virus genome comprises a first recognition site for a first restriction endonuclease and a second recognition site for a second restriction endonuclease; and wherein said first and second viral fragments are produced by digesting said viral genome with said first restriction endonuclease and said second restriction endonuclease, and isolating said first and second viral fragments.

100. The method of claim 99, wherein said first and second recognition sites are physically arranged in said genome such that the region extending between said first and second viral fragments is not essential for virus infectivity.

~~101. The method of claim 98, wherein said isolated virus genome is a herpes virus genome.~~

~~102. The method of claim 98, wherein said isolated virus genome is a poxvirus genome.~~

~~103. The method of claim 102, wherein said poxvirus genome is a vaccinia virus genome.~~

104. The method of claim 102, wherein said transfer plasmids and said first and second viral fragments are introduced into a host cell comprising a helper virus, wherein said host cell is non-permissive for the production of infectious virus particles of said helper virus.

105. The method of claim 104 wherein said helper virus is an avipoxvirus.

106. The method of claim 105, wherein said helper virus is a fowlpox virus.

107. The method of claim 99, wherein said first and second restriction enzyme recognition sites are situated in a thymidine kinase gene.

108. The method of claim 102, wherein said first and second restriction enzyme recognition sites are situated in a vaccinia virus HindIII J fragment.

109. The method of claim 108, wherein said first and second restriction enzyme recognition sites are situated in a vaccinia virus thymidine kinase gene.

110. The method of claim 108, wherein said first restriction enzyme is NotI, and wherein said first restriction enzyme recognition site is GCGGCCGC.

111. The method of claim 108, wherein said second restriction enzyme site is ApaI, and wherein said second restriction enzyme recognition site is GGGCCC.

112. The method of claim 103, wherein said isolated virus genome is a v7.5/tk virus genome.

113. The method of claim 103, wherein said isolated virus genome is a vEL/tk virus genome.

114. The method of claim 102, wherein the 5' and 3' flanking regions of said transfer plasmids are capable of homologous recombination with a vaccinia virus thymidine kinase gene.

115. The method of claim 114, wherein the 5' and 3' flanking regions of said transfer plasmids are capable of homologous recombination with a vaccinia virus HindIII J fragment.

116. The method of claim 114, wherein said transfer plasmids comprise heterologous nucleic acid molecules ligated into a plasmid selected from the group consisting of:

(a) p7.5/ATG0/tk,

(b) p7.5/ATG1/tk,

(c) p/7.5/ATG2/tk, and

(d) p7.5/ATG3/tk.

117. The method of claim 68, wherein said host cells are a monolayer, and wherein those host cells which have undergone a lytic event are released from said monolayer.

118. The method of claim 68, wherein said MHC molecule is a class I MHC molecule.

119. The method of claim 70, wherein said host cells are a monolayer, and wherein those host cells which have undergone a lytic event are released from said monolayer.

120. The method of claim 70, wherein said MHC molecule is a class I MHC molecule.--